

10/516768

Fig. 1

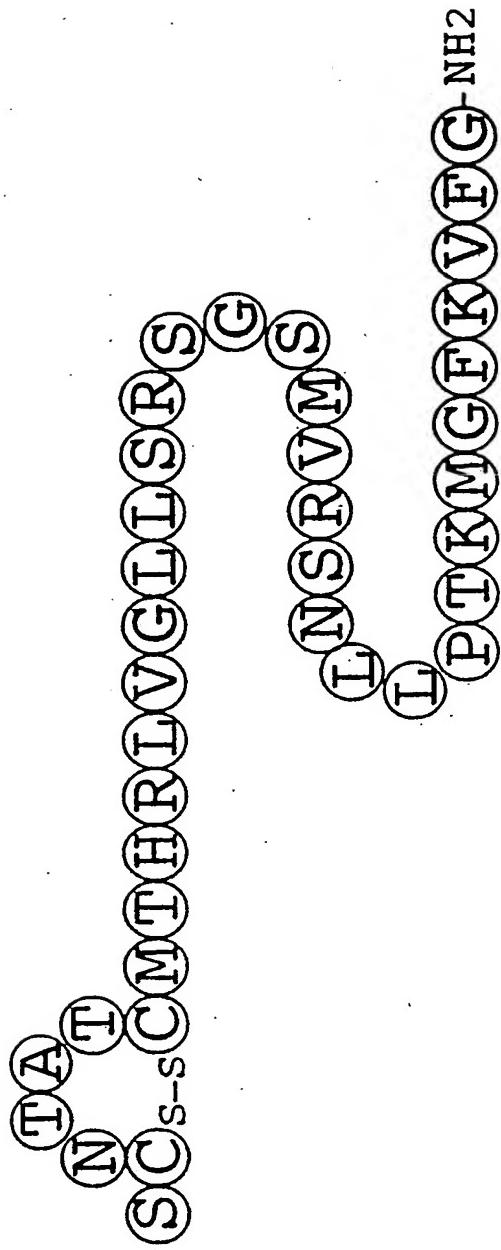


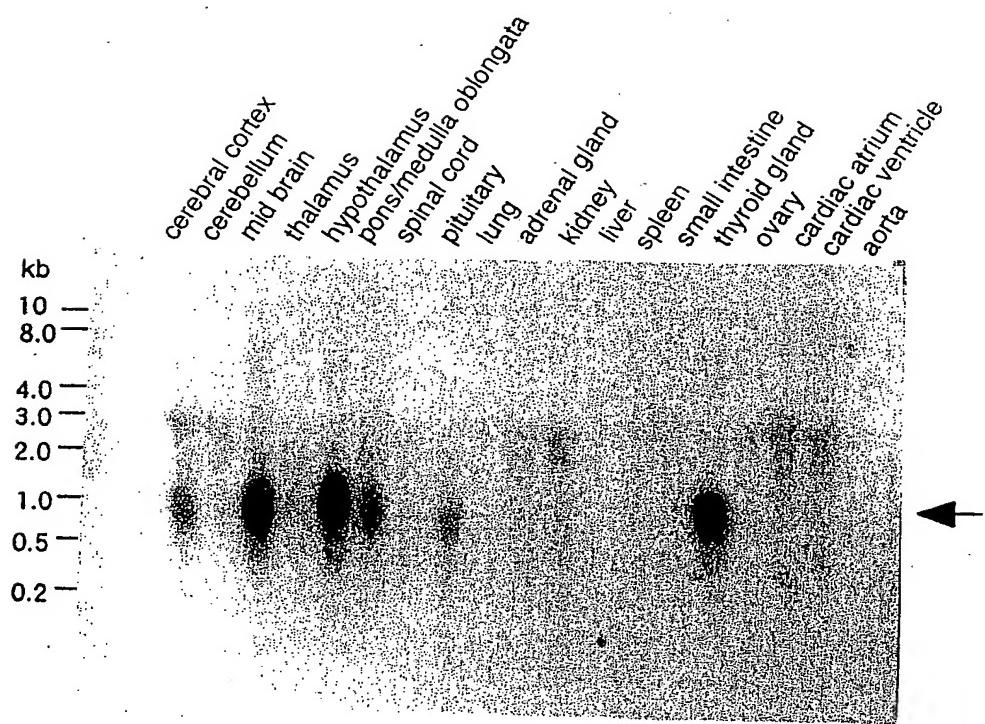
Fig. 2

SCNTATCMTHRLVGLLSSRSRSGSMVRSNLLPPTKMGFKVFG-NH₂
SCNTATCVTHRLAGLLSSRSRGGMVKSNFVPTDVGSEAF-NH₂
ACDTATCVTHRLAGLLSSRSRGGVVKNNFVPTNVGSKAF-NH₂
ACNTATCVTHRLAGLLSSRSRGGMVKSNFVPTNVGSKAF-NH₂
KCNTATCATQRLANFLVHSSNNFGAILSSTNVGSNTY-NH₂
CSNLSTCVLSAYWRNLNNFHRFSGMGGFPETP-NH₂
YRQSMNNFQGLRSFGCREFGTCTVQKLAAHQIYQFTDKDKDNVAPRSKISPAQGY-NH₂

PCRSP
PCGRP-I
hCGRP-I
hCGRP-II
hAmylin
PCT
hAM

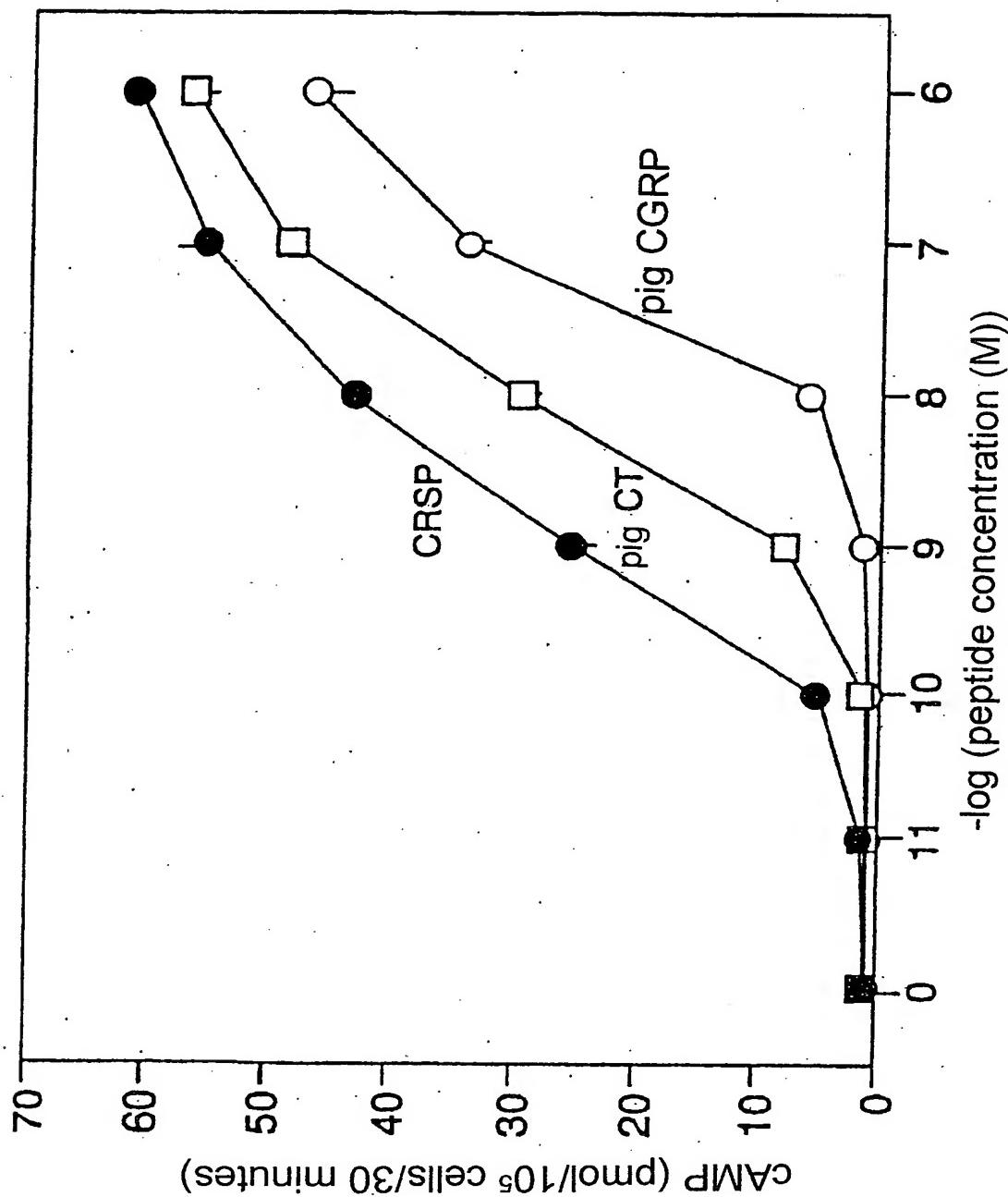
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Fig. 3



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Fig. 4



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Fig. 5

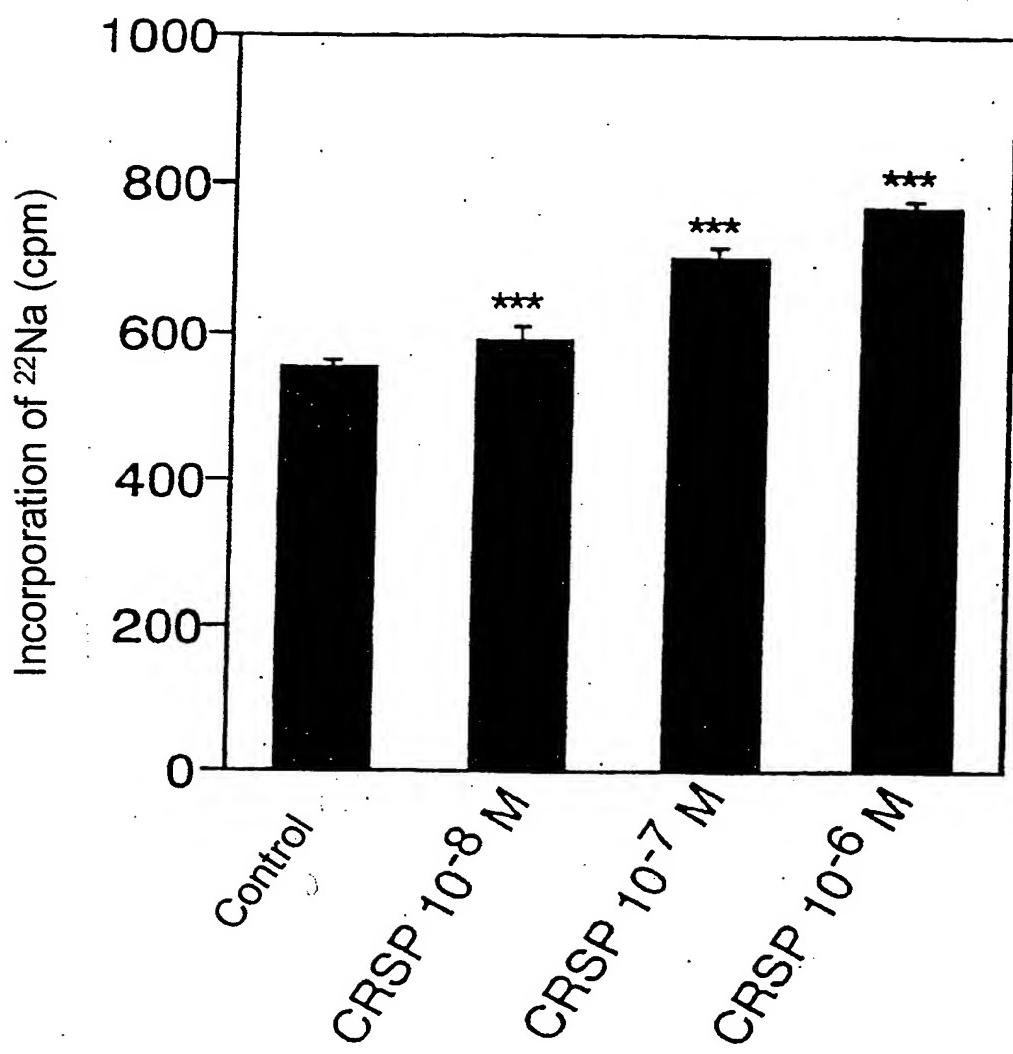


Fig. 6

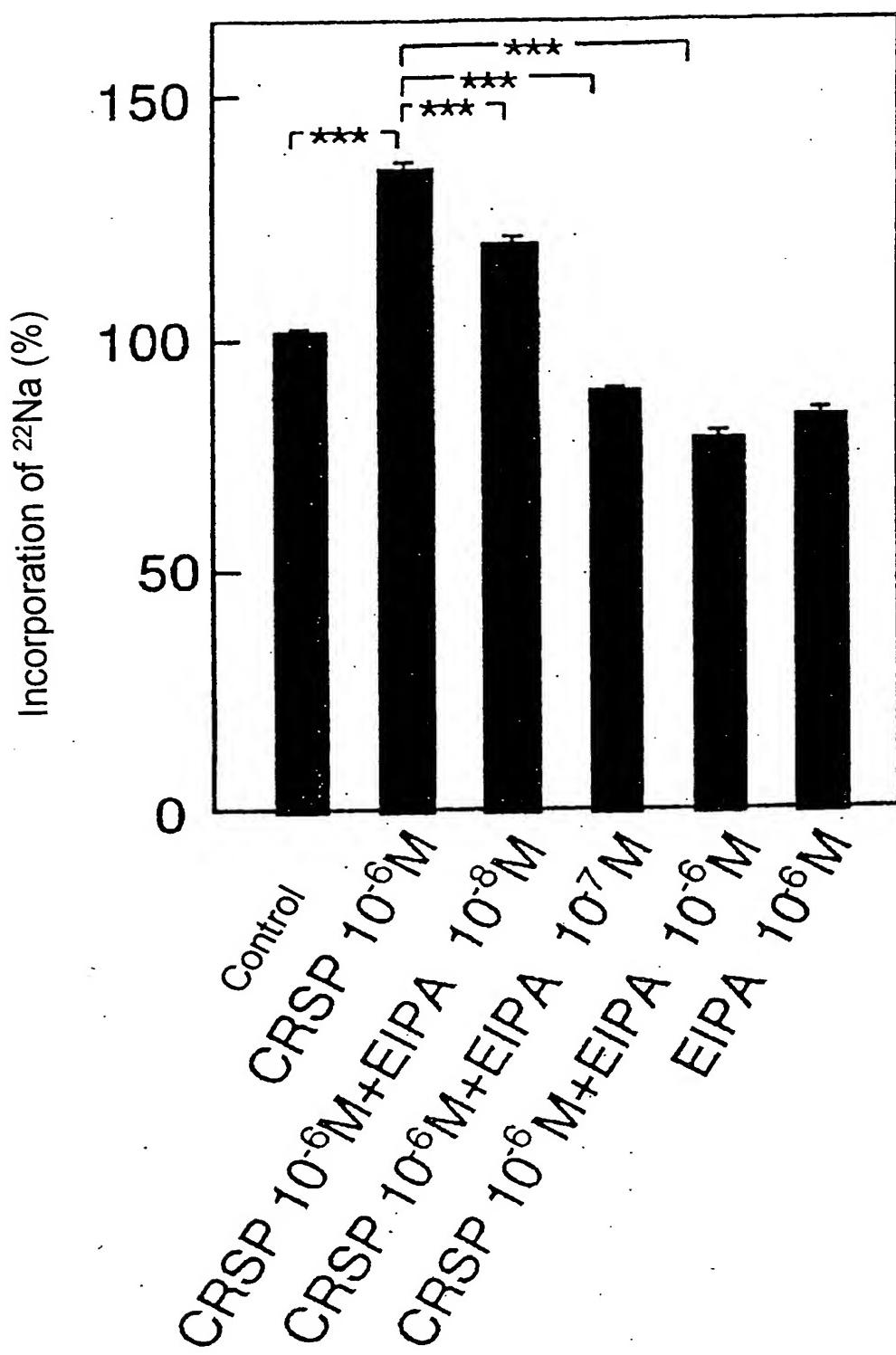


Fig. 7

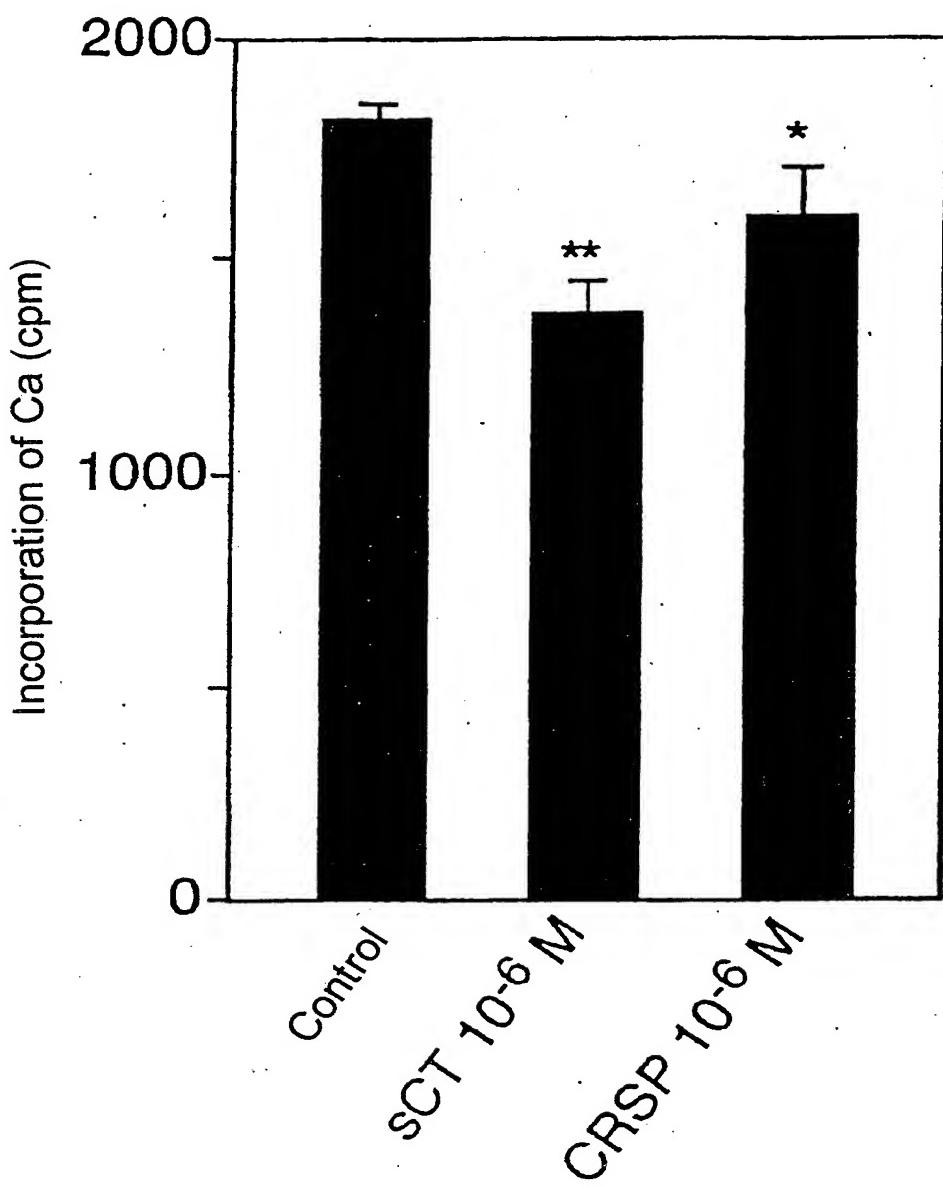
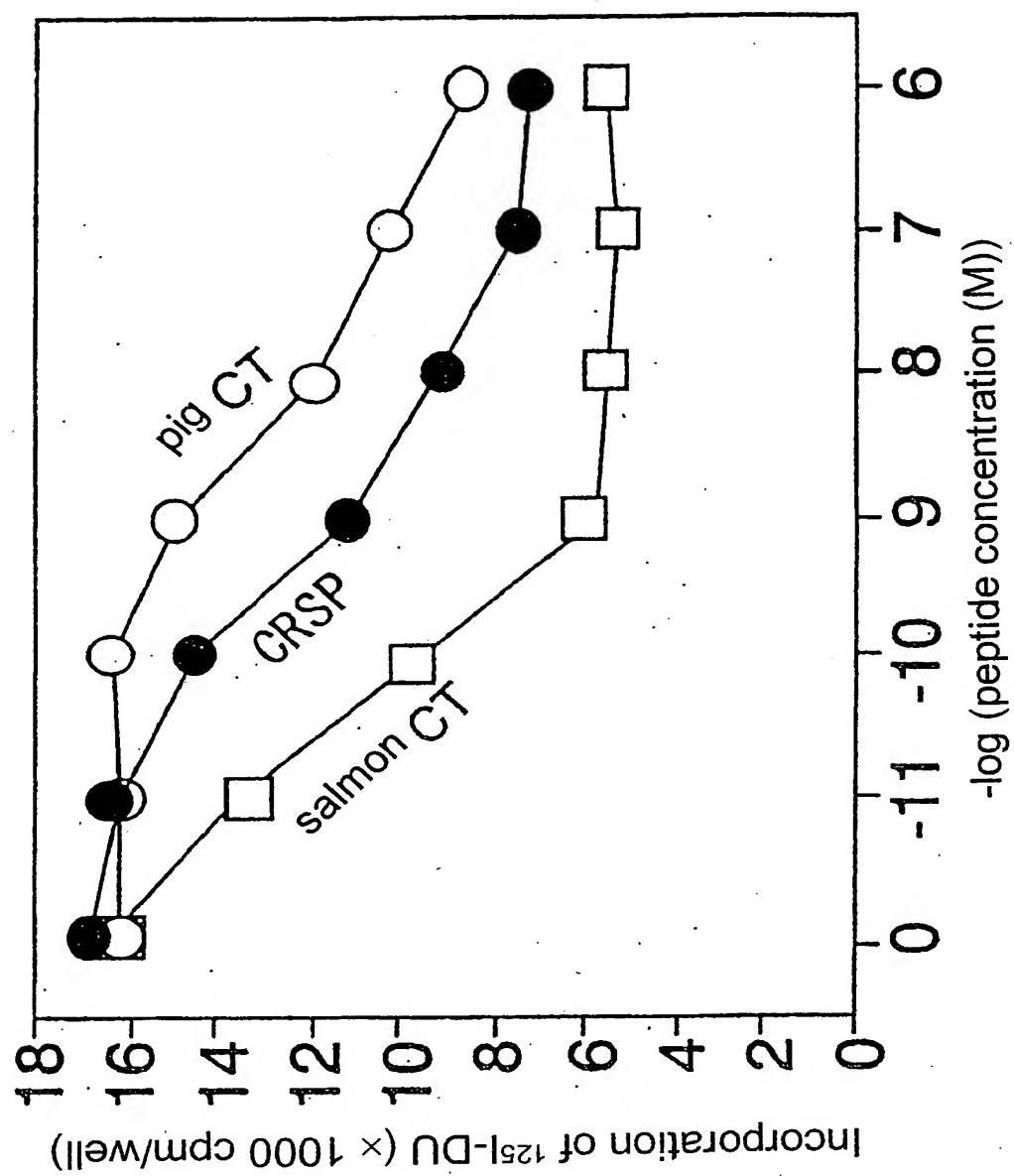
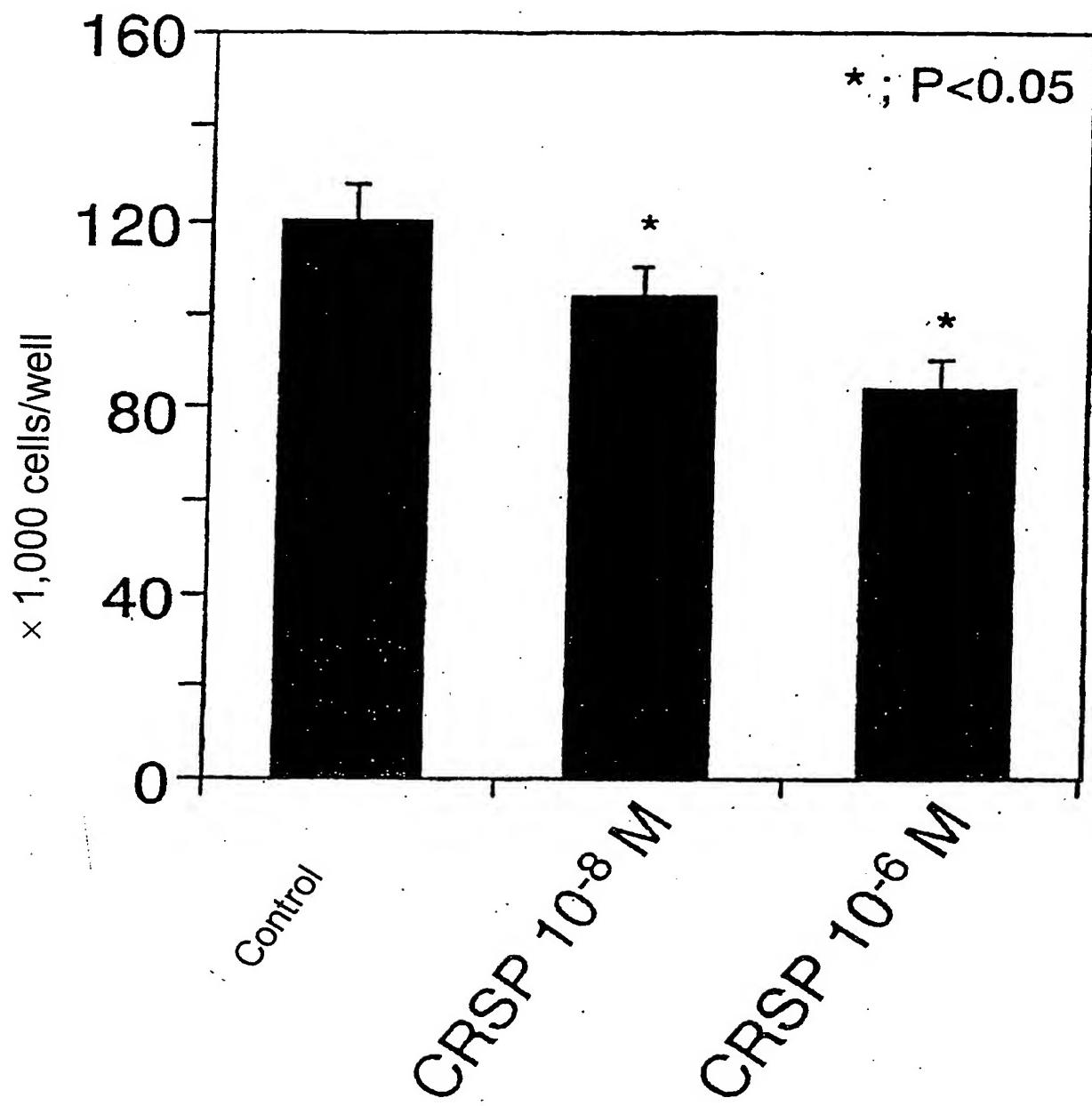


Fig. 8



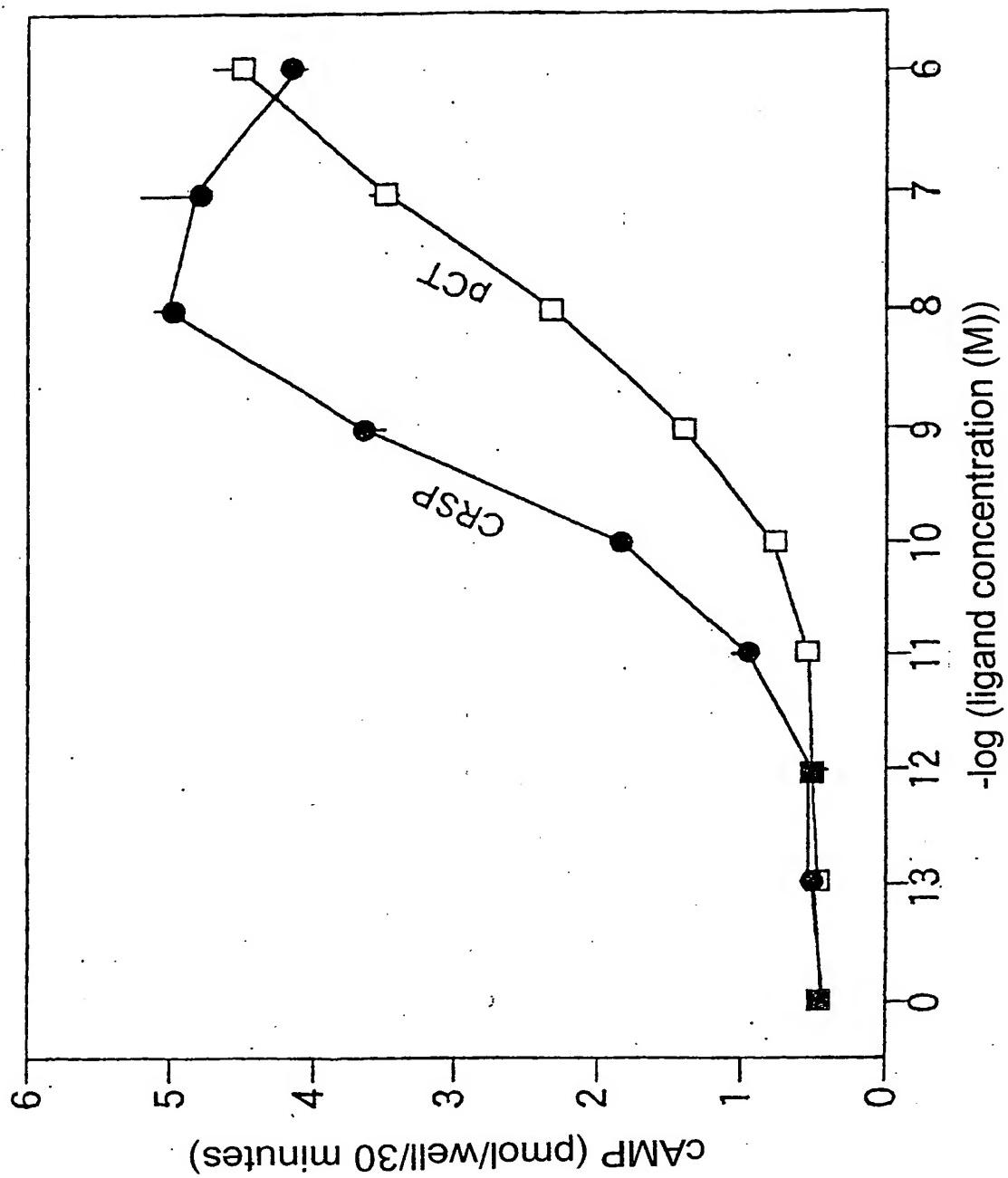
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Fig. 9



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Fig. 10



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Fig. 11

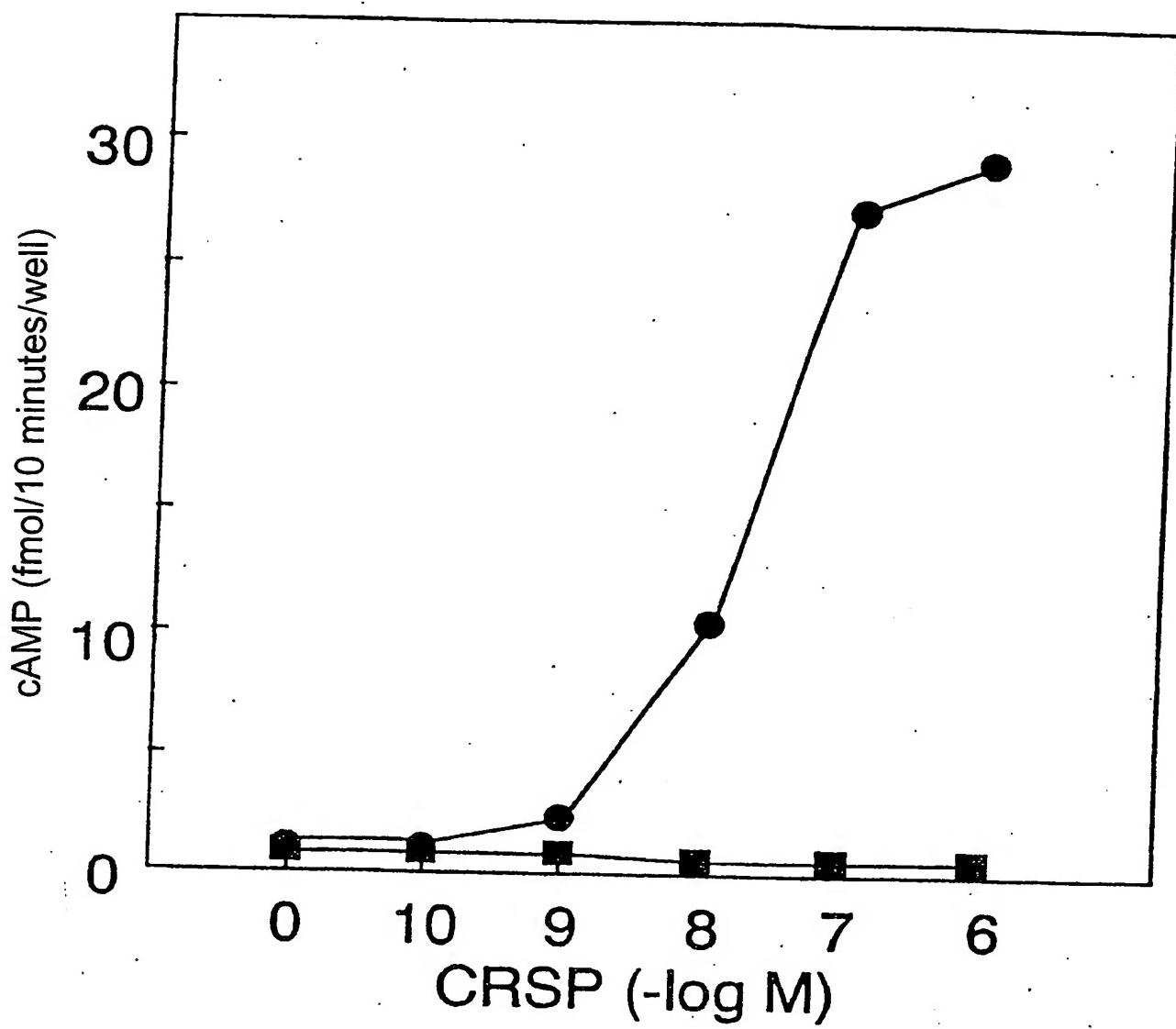
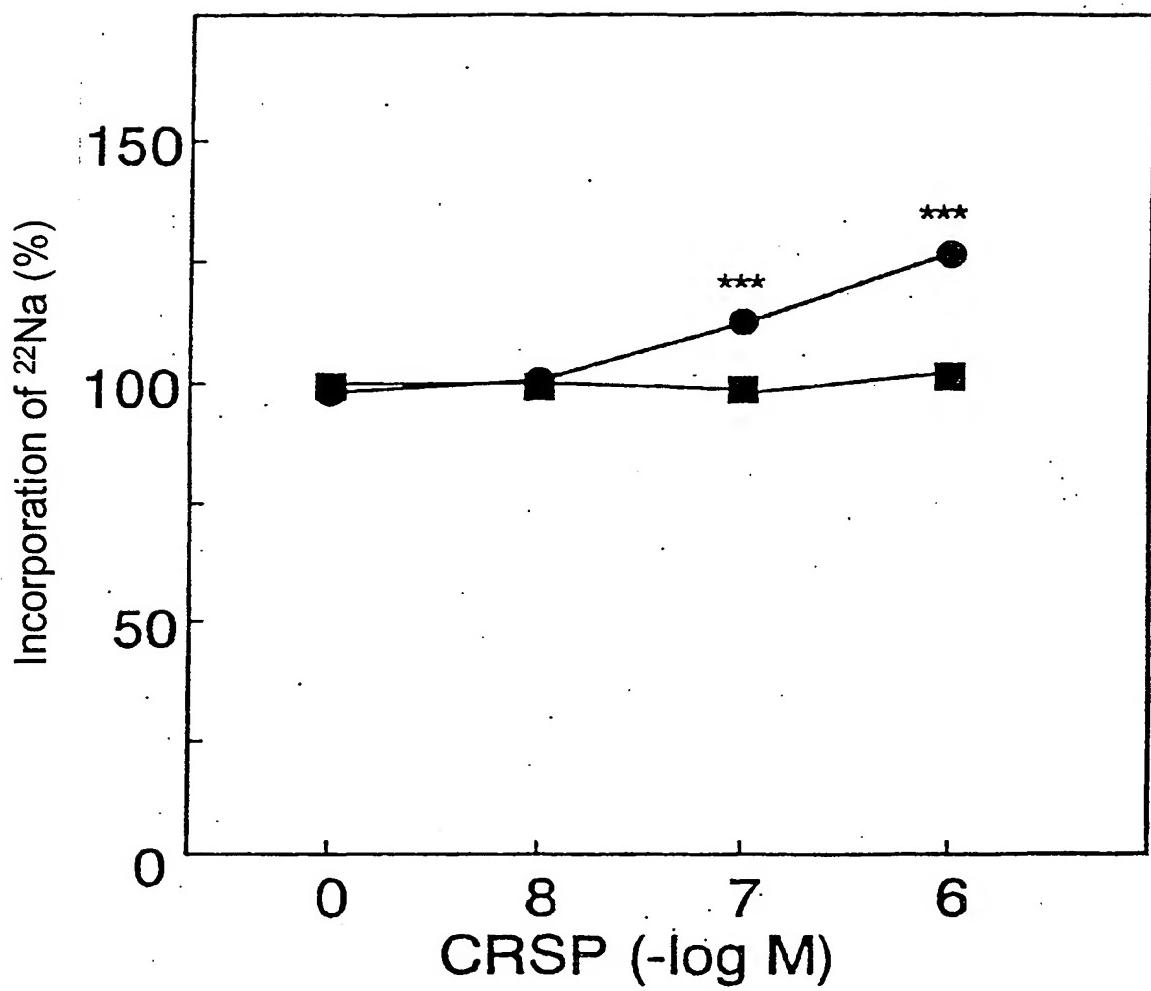
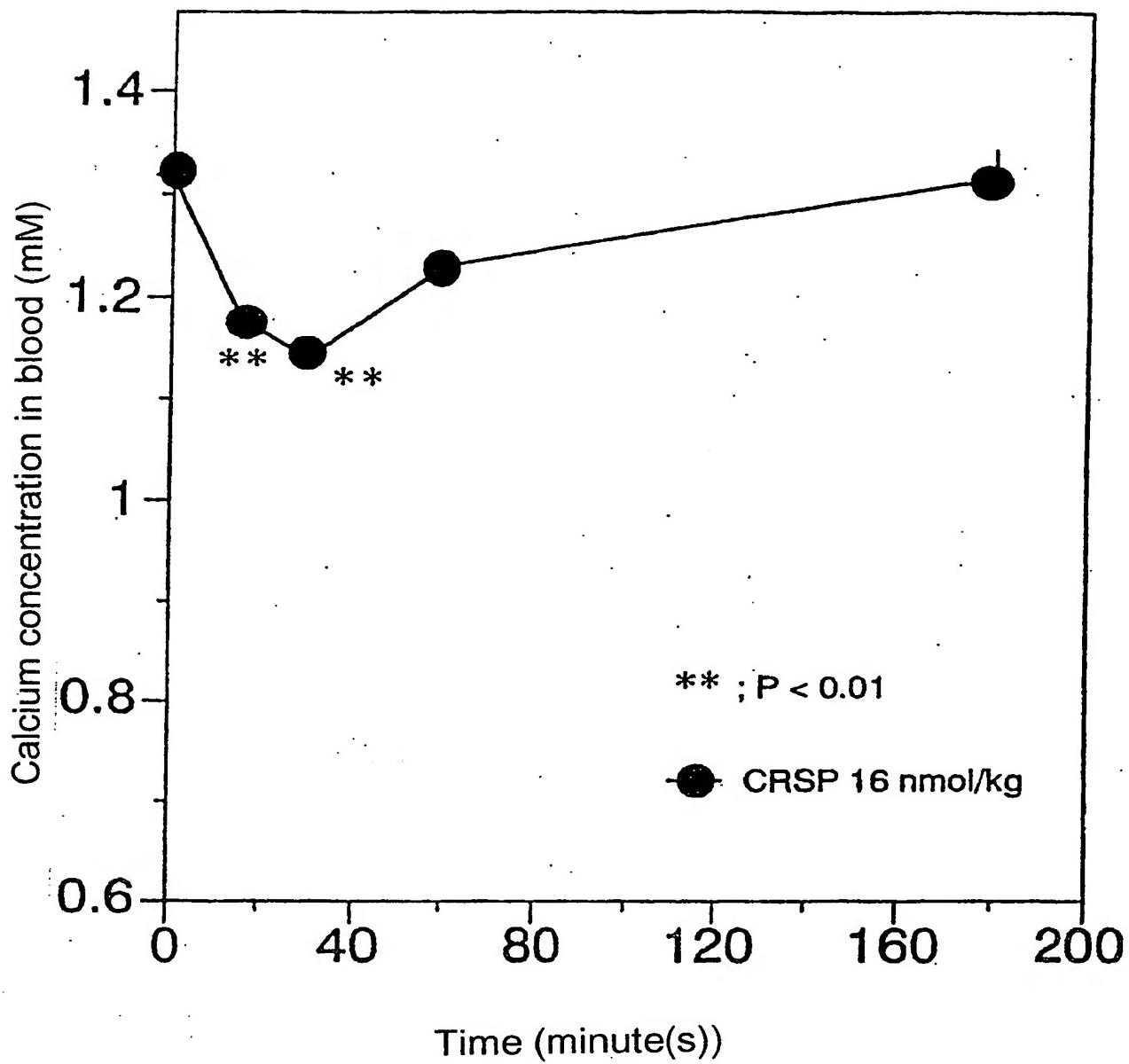


Fig. 12



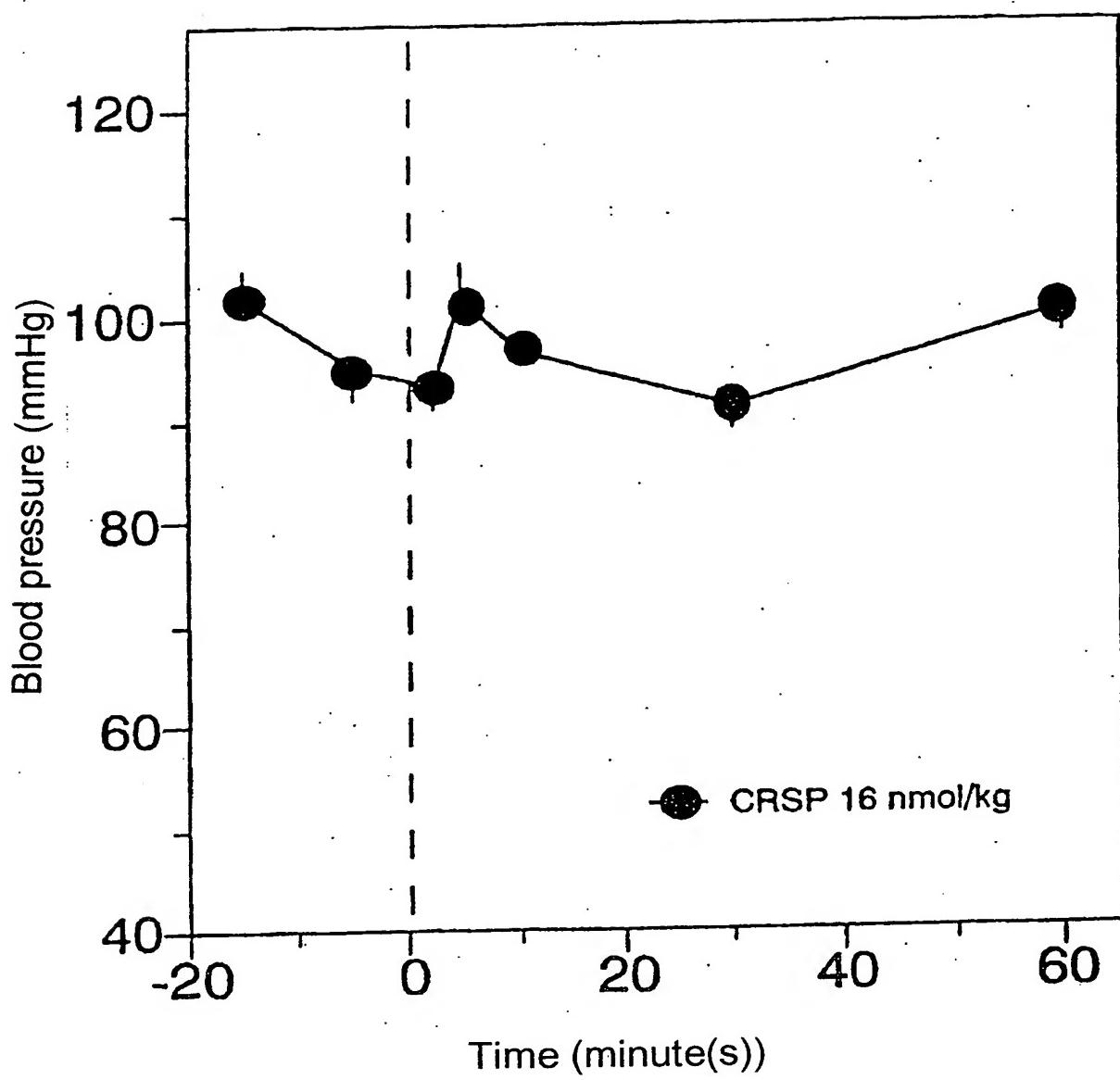
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Fig. 13



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Fig. 14



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Fig. 15

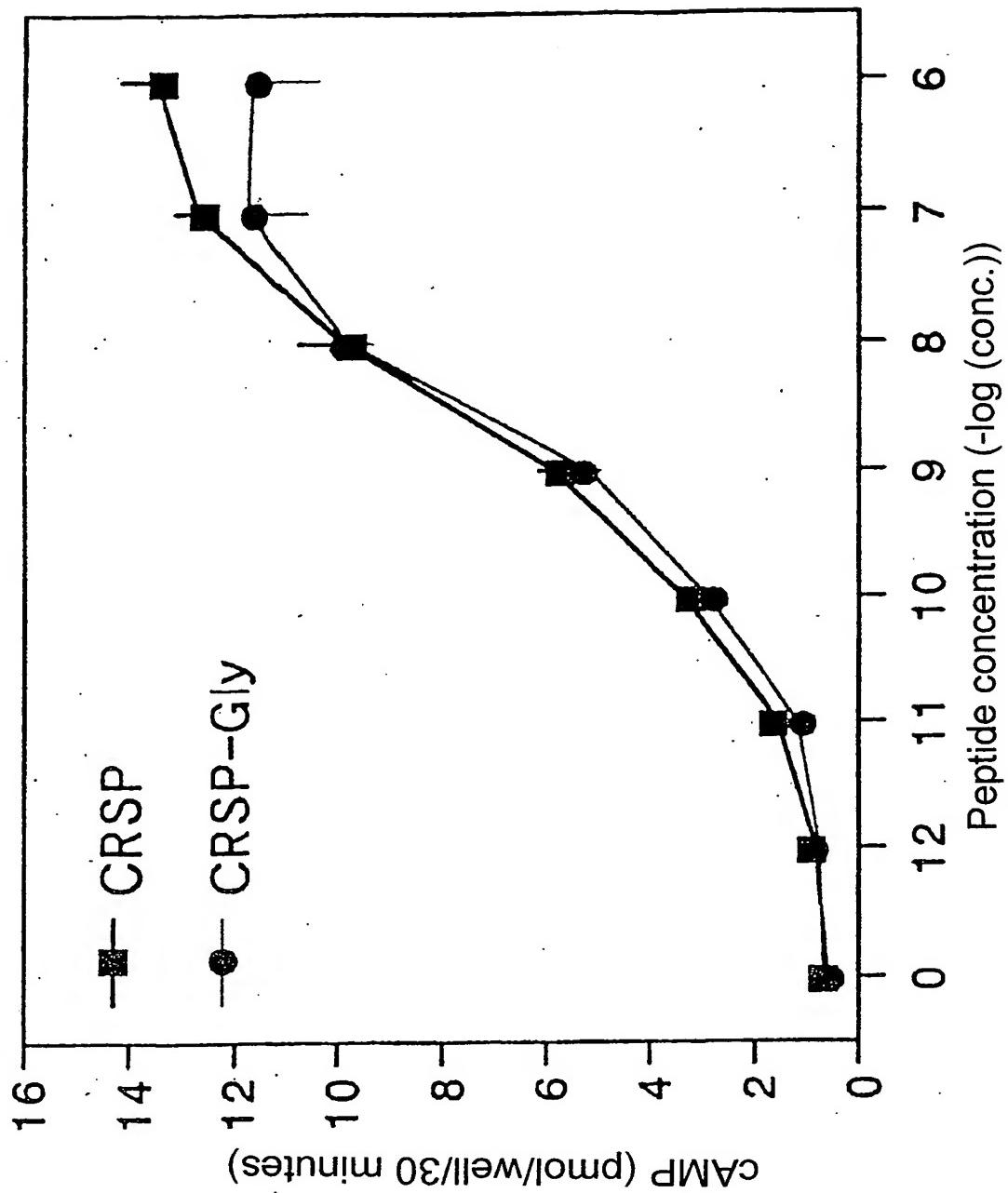
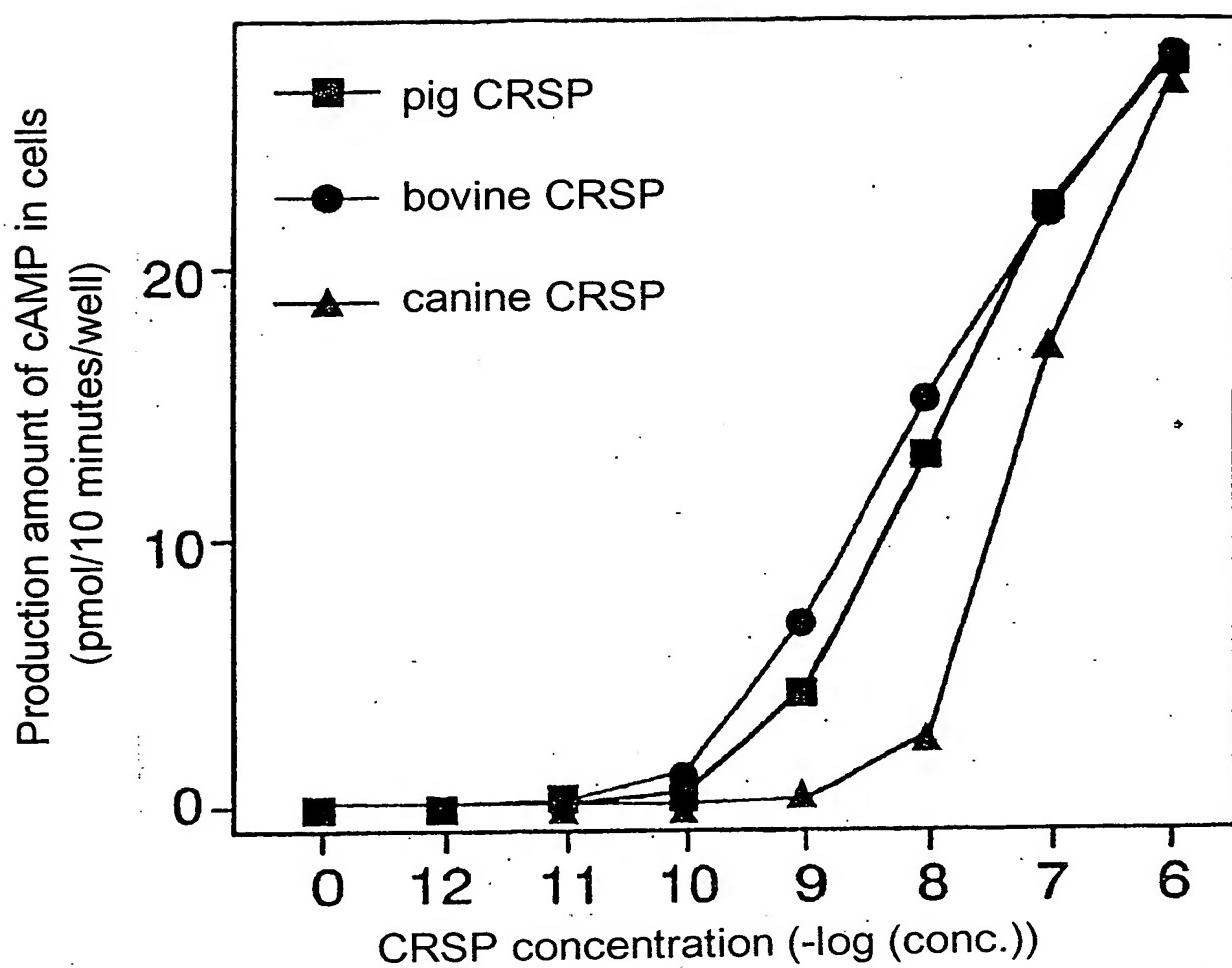


Fig. 16



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CTCGAGGATCCTGCCTTGTGTTCCCACAAATCCTGCCCTGTGCTTGATCCAGCTG 60
 CCTGAATCAGACCCCCCTGCTGGGCACAGAACATCAACCTGCTGCCATTAAACCTCCA 120
 AACCGCACTGGACATGGTAGTCTTAGGGGACGGGGATGCCCTGTAATGCTGGACTCTG 180
 CTCTACAAAGATCACATAGCTGGGATGGAGAGGGATGTGAGCCTGCAAACCGAACAGG 240
 TAAAGTTACCATGACGTCAAACGTCTAAATTCTGCTCACTTGCCTGTGTTTC 300
 GTTGGTGCCCACCAACCTCCCCACCCCTCCCACCCCGCCATCAATGACCTCAATGCAA 360
 ATACAAGTGGGGTGGCTCTGTTGGATGCTCCAGGTTCTGGACGCAAGTAGTGACACAATC 420
 CTGGGGCTCAGGATCTTCCTCTCATTGGTGCCTGGAGCTCTGGGACCACCCAGATTG 480
 AGAGCGGCGGAAATAAGAGCAGCTGCTGGTGCAGGGTAGAGGCACATACCCACCT 540
CAAGTGTCTCTGCCGCTTCCACAGTGCCTGACGCCAACGCTGCTGCCCTG 600
CTCCCTCCTCTGCTCCAGTCCACCTGGTCTGCTGCCGGTAAGCCGGAGATTCTGC 660
 TAAGCTGTGGTTCTGTTCTCTCCCTCTCCCTCTCTCCATTGGATT 720
 CTTAGCTGATCTCTTCTCCGTCTCAAAGTTCTGTCCACTCTCTCTGGTCTCTTCAT 780
 CCTGTAATATGCCCTACTGCGCAATTCAATTCTAGGCTCCTTCACAGGTAACTCTGGATG 840
 GTCTCAGTTCGGGGATTCCCTGCTACTCTCTGAGCTGAGCTGGGCTCCAGTCTGT 900
 CCCCGCAGCAGACGTGCTTAGGTCCTGTTGGGATTGGAGCTCTCCAGGCACTTCAGG 960
 GAGAGGAGGATGCAAGAATAGCTTGAGCAGAAGAAACTTCTATGGATCCCATCTCCTCT 1020
 TACCTACAAGGATCGCTGGAAATGGGGTCCGGACCTGGGACAGTGCAAATGGGTGGCAA 1080
 TAGGTGCAATGACTGAGGGGAAAGTAGCTATTAAACGCAAGCCCCAGTTGAAGGTTCTGG 1140
 GAACTCCCCCTCCCGACCGCCACCCCATTTAATCTTGGTCCAATTAAAGGCTGTACC 1200
 AGCTTGTCTTCTACAGGGTGTCTTGCCAGAGTATGGAGCAGCTGGACAGTAAAATTG 1260
 GTTCTCAGTTCTCAGGGATTCCAAC TGCAAGAGATATGTCCTCCAACTCCCCCTTCCC 1320
 CCAGCCAGGTATAAGAAAAATCAGGCATCAGGAGAGATGCTGATGGGTGCACTATGGG 1380
 AAAAGCTGTGGTGACAGGTACTGCGAGTCTGCTCCAGGAGTCCC GGCAACAGGTTGA 1440
 AGGTGAGAGTGTGGGTGTGCTGGCAGGGGGCTATGGACGGAGACCTCCTCACCCAGTTG 1500
 TCCTGCTAGGCTTCTTGCTAAACCAAACATGTTGCAGGCTCACTGGATCTTCCAGCAGT 1560
 CCACTGGCTGAGGAGGAAATGATGGTGAAGGAAAGGACACGAGCAGCCTGAAGCCAGG 1620
 AAGCCAGGGAGTTGGAGGCAGAGGCAGGAGCAGAGCCCAGGTCTGTGGCTCAATGAAC 1680
TGGAAC TGCTACAGGTGGTACATTGTTCTCCCTGCAAGAGGGCACCATGGCTTCTG 1740
MetGlyPheTr

GAAATTCCGCCCTTCTGGTCTCAGCATCCTGGCCTGTACCAAGGCAGGCATGTTCCA 1800
pLysPheProProPheLeuValleuSerIleLeuValleuTyrGlnAlaGlyMetPheHi

CACAGCACCAATGAGGTAAGACAGCCCTGCCAACAAAGCACACTCACTGATGAGAATGTA 1860
SThrAlaProMetAr

 ATATAAACGTGTATATAAATTATTATAAGGTGGCTCTGTAGAACAAATGGATAGTGCCTT 1920
 GCGCTCCTATAAGTTATCATAAGCTTATGTGTACACAAAGTTGTAATAGACATAAG 1980
 ATATACAGTACTCATGATTGTAATTTATATAACCTATCAAACCTCACAGCATGCTTTT 2040
 TTGTTTCTCAAAATATTGTACCTTGTACAGCACACGTATATGCTCATATTACCAATTAA 2100
 AGAAATGGATTGTATCCAATTGCCAAATACTTTGCTAGTAAATTGTTATTAATCTGA 2160
 TATGGGATCTACACATCTCATTTCACCTTCATTCAAACGTCAAGCTAAATTATT 2220
 TTCCCATTCAAACATCAGAAACCAGGCAACCTGGCTGTTATCCTGGGAGGGCAGGC 2280
 AGGAGATCAGAACCTGTTTAGGCTTCCCTCTAGGTCTGCCCTGGAGCCC 2340
gSerAlaPheGlySerPr

Fig. 17

(continued)

TTTGATCCTGCTACCCTCTGAGGAGGAATCACGCCCTCTGGCTGCAATGGTGAA	2400
<u>OPheAspProAlaThrLeuSerGluGluGluSerArgLeuLeuLeuAlaAlaMetValAsn</u>	
TGACTATGAGCAGATGAAGGCCCGTGAGATGCAGAACAGAGGGCACAGGGCTCCGGGTA	2460
<u>nAspTyrGluGlnMetLysAlaArgGluMetGlnLysGlnArgAlaGlnGlySerGly</u>	
AGGTTCCCTGCCCAAGGACAACAGGGCATCCCTTCTTCCTCTGGTCAGGCCAGGAAGG	2520
CATATTTAAAGTCACTTTGAGTTCTGACCCCCCTGGACATGTCTGGGATGATTA	2580
TGGCATTCCCCTGACGGCCTAGGATTTCTGCTGTGATGACCTTTCTAGCAGAAATAC	2640
TCAAGGTTCACTGGCCTCTCAAGGCAGTAGTCTTCCATGACGATTCTGCGTACAGCAC	2700
CTGCACTCAACCTCTCACTGACGGCCTTTCTTATCCCACAAATCAGCATCAGT	2760
<u>yIleSer</u>	
GTCCAGAAGAGATCCTGCAACACTGCCACCTGCATGACCCATCGGCTGGTGGGCTTGCTC	2820
<u>ValGlnLysArgSerCysAsnThrAlaThrCysMetThrHisArgLeuValGlyLeuLeu</u>	
AGCAGATCTGGGAGCATGGTGAGGAGCAACCTGTTGCCACCAAGATGGGCTTCAAAGTC	2880
<u>SerArgSerGlySerMetValArgSerAsnLeuLeuProThrLysMetGlyPheLysVal</u>	
TITGGTGGCGCCGCAGGAACCTTGGATCTGAGCAGTGGGATGATTCCAGGAGGAAGGT	2940
<u>PheGlyGlyArgArgArgAsnPheTrpIle***</u>	
GAATGCCCTTTGTACCTTCGGGTGGGAGGACAGAGGACTGGGTATTGCAGGGGTGCAT	3000
TCCACACCTAACCTCTGTGAGCGCATGGGGTAAACCTCCACATGCCAAGGTGCCA	3060
CACCAAGTGTCTGGAGAAAGGACTGATAATCCCTATAACTGAAACATTGGGCTTTCT	3120
CTGTTCTCCAGTCTCCCTGTGACACTGACATCATGCCAGGAAATATAGACCCCTGT	3180
TTACTTAAACACTGTTCCCTGGGTATTAATTGGGGTCCAGCTCTAGCATTAGAATTG	3240
AAGGTAATGACCCCTACCTTTGGAGCATACCTAACATGTTATGAACTGGAGCATAGA	3300
CTCGGATTCAAATACTGTCGCTCTCCACTAACTGACCATAGGCAAGTATGCCTCT	3360
GAGCCTCAGCTCTCTGTAACTTGAAGGCAACAATAGTATCCTCAATATAAAAATTAA	3420
TTAGTATAACATATGACAAGAGCCTGTTAACTAAGAATTAAATAACATTCTGTTACTTTT	3480
TCCCTCCTAGGTTACTATGACTCTGAACCTACTCGTTAAATTACAAATGAAAGCAACC	3540
TACTAAAAATAGCATGGAAGACATCCATGTATGCATGCTTCTGGAAACTGAAACACTC	3600
TTTCCTGAAATAAAACTAAACTAAATGCAAAATAAATCAATGCATCAATGCAAGTTAC	3660
CTTGTGTGCATCTTGTATATGATTCTATAATATGATGCATGTCTCATTAGGTTAA	3720
TGGTAGCAAATCTGGCCCTGTCAGCCAACCTGTTGGTGGGGCAGCTCTGCTAACCTC	3780
AGGGTCACATGAATT	3796

Fig. 18

GGATCCACTAGTTCTAGATAAAATGGACAAATACCTAGAAACAGAAGACCTACCAAGATG	60
GAAGGGATGAAGAAATAGAAAATTCAAATACACCTATGACTAGGAAGGGAGAATGAAGCATT	120
AATCCAAAATCTCCAACAAAGAAAAGCCCTGGATACGATGGCCTCATGGTGAATAGTA	180
CCAGACATTAAAGAAAACGAATACCAATCCTGTCAAACCTTCCAAAAACCTGAAGAG	240
AAAGGACACACCCCTAACCTATTCTATGAGGCAGGCCAACATTACTCTGATACCAAAGATG	300
GAGAAAGATTCTGCAAGGAGAAAACCCCTACAGACAAAATCCTTATGACATGGATGTGG	360
AAACCCCTCAACAGTATGCTAGGGATTGAATTCAAGCGTATTAAGGATCCTACAAC	420
ATGACCAAGTGGGATGAATTCTGGAATGCAAGGATGATTCAAAATATGAAAATTGATCA	480
AAGTGTATATCACAATAATGGAATGTAGGGAAAAACACACCTGATTATTCAC TGATA	540
CAGAAAATTATTTAGTAAATTCAATACCTTTCAGGATTAAAACAAAAACTAGGTATA	600
GAAGGAGACTGCCTCAGCACAATACAACACTATATATGAAAACCAACACCAACACCATAAT	660
CCAGGGTGGAAAACGTGAAAGCTTTCCCCTAAGATCTGGAAGAAAATGGAAAAAATTT	720
TAAGAATTTCAGACAGATTGGGCTCTGGTACACTCTGAGAAATCATCTTTAGAATT	780
TTTTTTTTAAAAATAAGCACAAGAATTCTATTAAAAGAAGGGAAATAACATAGCCTT	840
CAGAGTTATCAGGAGGTGTAATTTCACACTAGATTGTGGCTACCTGATGCTA	900
ATTTTGAGGTTAACATAATGAAATAAGATGTACAGCCAAGTGCCAGCTAGTCATGGA	960
ACTTTTACCTCAGTACTGTTAGTGCTTCAGCCTAAGAAGTTTCAGGGAGGGCTGCGTG	1020
CAATACAAGTAATCGGTACTTGCTGAAGGTCTAAATTCGAGTGCACCTGGTAAATCAG	1080
GGATGGGCGCAGAGGAGACTGGTCTGTAACTCAGACTAGTGAACCTAGAATTAGAAA	1140
GGGTACTTTGTGCTCCAAGCAAATCCTGTTACCTAACACTAGGTCCAATGCTCTGCAG	1200
GCTGTAGTTAGAGCCCTCTCATAGCAGGGAGACTGCCCTGGTGAATCTGCCAGAGGAAAT	1260
GAATTTCATTACATTCAACAAACATTGGCGAGTGCACCTCATGTGCAAACAA	1320
TGGTGCTAAGTGTCTAAAGAAAAGATGTTGTTGTAAACTTACCCGCAGCTCAGAGCCAG	1380
GACTTCTGGAAAGTCAGAGGACTTGAGGAAGGAGTTCATCTAGCCCCCTCCCTACTGG	1440
AGAGACTGGCTTTCTTCAGTAAAGCTAAAATGCTGGAGGCTAAGTTAGCACCCCT	1500
CTGGGGGAGACCCCTGATTCTGCCTCTCATCCCCAGCCCTTGTGTGGCGCAAAG	1560
ATTCTGAGTGAGGAATGAATGTTGGCTTGAACAGGAAAGGCACAAGTGGCAGCCAAGG	1620
GTAGAATGCTGAGCCTACAAATTAAACATAGTTACAAATTGTCTTCTAAAGGAGTCGTTT	1680
CTTAGCCATAGTGCAGCACCTTGCATTGATCAAACACTGTGGTCTTCCAATGAAAAAA	1740
GAATCCCCAGACACACATACTACAAATGATTCAAGAGATTGATAGGTGGAAATCTC	1800
AGGTTTGAGTTATTGCAAAAGCGTTTGCCTGAGTTAAACTTTTTTTT	1860
TTTTTTTTGTATTTTCACTCTAGGGCGGCTCGGGCGCATATGGAAATTCCAG	1920

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GCTAGGGGTCTAATAGGCCCATAGCCACCGGCCTACGCCAGAGCTACTGCAACGCTGGA	1980
TCCGAGCCGCATCTGCAACCTACACCACAACACTACGGCAATGCCGGATCGTTAACCCACT	2040
GAGCAAGGCCAGGGATCGAACCCGCAACCTCATGGTCTTAACCTCAGATTGTTAACCACT	2100
GCGCCACGACGGCACTCCAACCTACCAAGACTCTTAATTAGTAGCAGAGTCCAATTAC	2160
ATGCCGCACCATCTGTTACCCGAGTTAGCGAACTGGTCTGGAACCTAACTCCTCAC	2220
GGAAAGCCAAGCCGAGTACTCATATTATAGTGCTAACCCCCAAACCCCTGGTCTGGCCT	2280
GTGCACCCAATTGGCTTGTTAGTAGAAACCAGGATTACGGAGCCCAGCAGTCCGCCA	2340
TCCTGAACTCTTCTCTTCACCTGCCTTCATCCTGGAGTGCACCTGCCCTCTATGAA	2400
CCAGTTTCCGTCCTGGTCTCCGATCCGTTGCTATCCTGAGGAGAGCAGATGC	2460
AAGCACCCGATTCCCTAGCCCCAATATTCTCTGCAAGGGAGAAAAGTTGAATAA	2520
GGGTATCTGTAATGAGATGTTCCGAGTCCAGAGAGCACAAACCGCAAGGGAACAGA	2580
TGTGCCCGAGGCAGGTGTGCGAAAGATATAGAGAAGGCTCAGGTTCGACCTGTGGCT	2640
CAGGTACACACTCATGGCAGAGTCGGTTAACCTCGGCTCTGCCTGGGGAACCACTAA	2700
CTGGGGTCTTGCTGCCCTCACCGCCCCCGATGCTGTTGCAGCGTTGCCGCTGGA	2760
GGGTCTGTACAGGCTGCTGCCGTTATCGCTGTGCTCAGACACGGTGTACCTGAGCAG	2820
CATCCGAACGGATTGGGGTAGATGTGGGCACAGGGCTGGAATCACAGGTCACTGGAACA	2880
TCTTGGCAAACAGCAGCCGAAGCAAGGGCAGCTGGCAAATGGTCTGGACATTGAT	2940
GGGCTTAGATGATGAATGGTGGGGCTGGAGGTGGCTGGCGCTGGGAAGCATCTATG	3000
CCGTGCACGTCCCTGCCAACGCCAGTAGGGCACCATTTCCCATATGGTGGACCGAC	3060
CACCCAGCGCGACTCCAGACATCCGCACAGAGGTGGGATTGGCAAATGGATCGCGATC	3120
GCACAGAACATCCCCTCTGCACTTCCCTGGTAAGCTCTCGATCCCTCCCTGGGTGGAGA	3180
GCAGGTACATGGCTACTAATGATACCACTCCTGAAGACGGAAATATGATGCCCGTTCC	3240
AAAAATTAATATATTGAGGTGCTAGAACAGACTAGCCGATGATCTTACCTACAGAAAA	3300
GGCACAGCTGGAACAAAGTTCCGTGACAAAGACTGTGATCCTGCCTCTGTTCCCA	3360
CAAATCCTGCCCTCTGTGTTGATTCCAGCTGCCGTGAATCAGACCCCCCTGCTTGGCAC	3420
AGAATCATCAACCTGCTGCGCATTAACCTCCAAACCGCAGTGGACATGGTAGTCTTAG	3480
GGGACCGGGGATGCCCTGTAACGCTGGACTCTGCTCTACAAAGATCACATAGCTGGGAT	3540
GGAGAGGGATGTGAGCCTCGAAACCGAACAGGTAAAGTTACCATGACGTCAAACGT	3600
CTTAAATTCTGCTCACTTGCCTGTTGTTGCTGCCACCAACCTCCCCACCC	3660
CTCCCACCCCGCCATCAATGACCTCAATGCAAATACAAGTGGGGTGGCCTGTTGGATG	3720
CTCCAGGTCTGGACGCAAGTAGTGCACACAATCCTGGGGCTCAGGATCTTCCTCATT	3780
GGTTGCCCTGGAGCTGGGACCAACCCAGATTAGCAGCGGGAAATAAGAGCAGCTGCT	3840

Fig. 19

GGTGCGGGGAAGGGTTAGAGGCACTACCCACCTCAAGTGTCTGCCGCTCTTCCACAG	3900
TGCCATCGCCTGACGCCAACGCTGCTGCCCTGCTCCCTCTGCTCCAGTCCACCTGG	3960
TTCCTGCTGCCCGGTAAGCCCGGAGATTCCCTGCTAAGCTGTGGTCTGTTCTCTCTCCC	4020
TCTCCCTCCCTTCCCTCTCTCCATTGGATTTCTTAGCTGATCTCTTTCCCGTCTCAA	4080
AGTTCTGTCCACTCTCTCTGGGTCTCTCATCTGTAATATGCCCTACTGCGCAATT	4140
ATTCTAGGCTCCTTCACAGGTAACCTCTGGATGGTCTCAGTTGGGGATTCCCTGCTCTA	4200
CTCTTCCGTAGCTGAGCTGGGCTCCAGTCTTGTCCCCCAGCAGACGTGCTTAGTCCGT	4260
GTTGGGATTTGGAGCTCTCCAGGCACCTCAGGGAGAGGAGGATGCAGGAATAGCTTG	4320
GCAGAAAGAAACTTCATGGATCCCATCTCCTCTTACCTACAAGGATCGTGGAAATGGGG	4380
TCGGGACCTGGGACAGTCAAATGGGTGGCAAATAGGTGCAATGACTGAGGGGAAAGTAG	4440
CTATTAACGCAAGCCCCAGTTGAAGGTTCTGGGAACCTCCCCCTCCCGCACGCCACCC	4500
ATTTAATCTTGGGTCCCAATTAAAGGCTGTACCGGCTTGTACAGGGTGCCTT	4560
CCAGAGTATGGAGCAGCTGGACAGTAAAATTGGTTCTTCAGTTCTCAGGGATTCCAAC	4620
TGCAGAGATATGCTCTCCAACTCCCCCTCCCCCAGCCAGGTATAAGCAAAATCAGGC	4680
ATCAGGAGAGATGCTGATGGGTGGCACTATGGAAAAGCTGTGGTGACAGGTACTGTGAG	4740
TCTGTCCTCCAGGAGTCCGGCCAACAGGTTGAAGGTGAGAGTGTGGGTGCTGGCAG	4800
GGGGCTATGGACGGAGACCTCTCACCCAGTTGTCTGCTAGGCTTCTTGCTAAACAA	4860
GCATGTTGCAAGCTCACTGGATCTCCAGCAGTCCACTTGGCTGAGGAGGAAATGATGGT	4920
GAAAGGAAAGGACACGAGCAGCCTGAAGCCAGGAAGCCAGGGAGTTGGAGGCAGAGGCAG	4980
GAGCAGAGCCCAGGTCTGTGGCTCAATGAACTTGGAACTGCTACAGGTGGTGACATTGT	5040
TCTTCCCTTGCAGAGGGCACCATGGGCTCTGGAAATTCCGCCCTGGTCTCAG	5100
MetGlyPheTrpLysPheProProPheLeuValLeuSe	
CATCCTGGTCTGTACCAGGCAGGCATGTTCCACACAGCACCCGTGAGGTAAGACAGCAC	5160
rIleLeuValLeuTyrGlnAlaGlyMetPheHisThrAlaProValAlr	
TGGTGGCAGTGCCTCGCTTCCCACGGCCCCCGGAATCATATAGTTCTGTATTGTGAGTT	5220
GTGCTGTGGTGAGTCTGGCTCTGGTGGCTCTGTGTATAGGGGGTGTGGGTCTAAT	5280
GTATGAATATAGTCATGTATATAAGTTATTATAAAATATTGTGATCCAAGATAATATC	5340
ACAAAGTTACAAATAAGAAGATATAACAGTATTCACTATAAAATTCTAAACTCACTG	5400
AACCTTACAGCATGTTTGTGCTTTATGAAATGTTATAACTTTAGCAAACCTATA	5460
TAGTAATTAGCCATAATTGAGCAATGAATTGCATTCTAATAAGTAATTGTCAATAA	5520
ATTTGTTATTAAATCTGAAAGGTATCTATACAATTCTCACCCCTTTCAAATTATATT	5580
AATATGAAACCATTTCATATTCAAACATCATTAAATTAAATAATGGCTGTATTAA	5640
CACTAAGCTCATACAATTCTGAAGATCTAACCATCAGCTTCAAAAGCCTACATGATGC	5700
ACTTTCAGCAGAACTACTTGTGGACACCCAGAGCCTAACTCATGGTGAAGCAGCATT	5760
TTGGATGAACACTAGCCTTATGCTCTGACC GTGAGAATTCTCATCAGCTTATTCTCAGA	5820
GGAAGTGGCAGAAACCAGGAAATCTGGCTGCTTATCCTAGGGCTGTGGTAGGCTCAGAGC	5880
GCATGTTGGGCTTGCCTTCCCTCCAGATTGCCTTGGAGAGCAGCTTGATTCTGCCA	5940
gLeuProLeuGluSerSerPheAspSerAlaT	
CTCTCACAGAGGGAGGAAGTGTCCCTCTACTGGTTGCAATGGTGAAGGATTATGTGCAGA	6000
hrLeuThrGluGluGluValSerLeuLeuValAlaMetValLysAspTyrValGlnM	

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TGAAGGCCACTGTGCTGGAGCAGGAGTCAGAGGACTCAGGTCACTTGCACCCCTCC <i>etLysAlaThrValLeuGluGlnGluSerGluAspPheSe</i>	6060
CAGAATATGGCTTACCCCTCCCTAGAGTACCGAGGAAGGCATATCCTTAAGAACATGAGATT TGTTATAGTGCCTATAAGCCTTGATGTCCAGTCATCATAAGCCTGGTTATTTTAGTTA TTACACAGGAGAGATTGTCTATTACAGTTCTGATTTCCAGGTCAGTAATGCAGAGCCAC CTTGCGGTTCTGACACCCCTGAAAATGCTATGGGGAGTGTGATGCATTTCAGGTTCACTGGTC AGCCCTATGGTTCTGTTGGGATTTGTGTTAGCAGAAACATTCAGGTTCACTGGTC CCTCTCAGAGCTGTAATTTCACGTGATGGTCAGTCCTGGGGGAATCACTGCCCTCAA GCTGTCATTGGCAGGCCTCTCTTGTCTCCATCCTGAAAATCAGCATCACTGCCAGGA <i>IleThrAlaGlnGl</i>	6120 6180 6240 6300 6360 6420 6480
GAAATCCTGCAACACTGCTAGCTGTGACCCACAAGATGACAGGCTGGCTGAGCAGATC <i>uLysSerCysAsnThrAlaSerCysValThrHisLysMetThrGlyTrpLeuSerArgSe</i>	6540
TGGGAGCGTGGCTAAGAACAACTTCATGCCACCAATGTGGACTCCAAAATCTTGGGCTG <i>rGlySerValAlaLysAsnAsnPheMetProThrAsnValAspSerLysIleLeuGly**</i>	6600
<u>ACGCCGCAGAGAGCCTCAGGCCTGAGCTGTGAAATGACTCCACAAAGAAGGTGACTGCTC</u> *	6660
TAGAACATGGGATAGCAGGGCAAATGGCTGGGTATTCAGGGGTGTTGGCTACACTCTAA CCCTCCCTGAGCCTGTACTGAAAAAAAAATCCATAATGAAGTGTGACCCCCATTATCC TCAGAAAGAAAAGAGAACCTTAATAGCCAAAACCCCTATAACTAGGTTCATTTCTATT TTTCCAGTGTCTCCAGTGACTCTGAGGTCACTGTCAGGAAACATAGATTCTATTCTT TTTCTTTCTTTGGCTACACCCAAGGCATGTGAAAGTTTGGGCCAGGGATTGAAT CTGAACCATAGCTGTGACCTATGCAGTACCTGTGGCACACTGGATCCTAACCCAATGT ACCACATCAGGAACCTCTAGGTCTATTATTAAAACACTGTTCCCTGCAGTTATAATTG TGATTATTCTAGTTTGAGTTGAAAGGTAAATGATCTTATCCAGTGAGTTGAAGTATA ACTACAATGTCACATATACTGAAATTAGCAGAGCATTGACTTGGTTCAAATGCGATGTCTG TCTTCCACTAACTATACAACCATGGCCAGACCCCTCTGAACCTCAGTTCTACATGAAA CTTTAAGGCAACATAATATTACCTGTTATCATTAATATAAAAAGTAACTGAGATAATT CATGGTAAGAGCCTCACTATTAAAGTAATAATATTCTAGCTCTTATTTTTCTCC TAGGTCAACCAAGGAAACTGAACCTATTCTTAAATCTGCAATGAAAGCAATTATTTGA AAAATAGCATGGAAAACACACATATATGCATGCTTCTGCTTGAATACAGCTTTAGCT TGAAAATAAACTAAAACATGCAGAATAAAATCATTGCACTACCTGATATGTATCATT TTAATATTGATTCTGTATTCTATAAGTATGACTCATGTCGCTGGCTATCTGGTAGC AAATCTGGACCCCTGTCAGCCAACCTGTTGGTGGCAGCTCTGCTAAACCTC	6720 6780 6840 6900 6960 7020 7080 7140 7200 7260 7320 7380 7440 7500 7560 7620 7673

Fig. 20

CTCAAGTGTCTGCCGCTTCACAGTGCATGCCCTGACGCCAACGCTGCTGCCCTC	-52
TGCTCCCTCCTGCTCCAGTCCACCTGGTTCTGCTGCCCGAGGGCACCATGGGCTTC	9
	M G F 3
 TGGAAATTCCGCCCTCCTGGTCTCAGCATCCTGGCCTGTACCAGGCAGGCATGTC	69
W K F P P F L V L S I L V L Y Q A G M F	23
 CACACAGCACCCGTGAGATTGCCCTTGGAGAGCAGCTTGATTCTGCCACTCTCACAGAG	129
H T A P V R L P L E S S F D S A T L T E	43
 GAGGAAGTGTCCCTACTGGTGCAATGGTAAGGATTATGTGCAGATGAAGGCCACT	189
E E V S L L V A M V K D Y V Q M K A T	63
 GTGCTGGAGCAGGAGTCAGAGGACTTCAGCATCACTGCCAGGAGAAATCCTGCAACACT	249
V L E Q E S E D F S I T A Q E K <u>S C N T</u>	83
 GCTAGCTGTGTGACCCACAAGATGACAGGCTGGCTGAGCAGATCTGGAGCGTGGCTAAG	309
<u>A S C V T H K M T G W L S R S G S V A K</u>	103
 AACAACTTCATGCCACCAATGTGGACTCCAAAATCTGGCTGACGCCGAGAGAGCCT	369
<u>N N F M P T N V D S K I L G</u>	117
 CAGGCCTGAGCTGTGAAATGACTCCACAAAGAAGGTACCAAGGAACGTAACTCTATTTC	429
TTTAATCTGCAATGAAAGCAATTATTTGAAAAATAGCATGGAAAACACACATATATGC	489
ATGCTTCTGCTGAAATACAGCTTAGCTTGAATAACTAAACTAAATGCAGAATA	549
AAATCATTGCAGCTACCTGAAAAAAAAAA	579

Fig. 21

GCCCAGCTTACGTCTCCITTCTCCGCCAGTGCATCACCTGCCACCAGCGCGGTTGTTGC	-52
TTCTCCCACCTGGGCTCCAAGCTACCTGGTCCTGCATCCAGAGGGGACCATGGGCTTC	9
M G F	3
TGGAAGTTCCCCCCTTCCTGATCCTCAGCATTGCTGAGCTTGTACCAAGCAGGAATGCTC	69
W K F P P F L I L S I L V L Y Q A G M L	23
CATGCCGCGCCATTCAAGGATGGCTTGGAAGCAGCTTGTACCTGCCACACTCACGGAA	129
H A A P F R M A L G S S F D S A T L T E	43
GAGGAAATGTCCCTCCTACTGGTGCATGGATTATGTGCAGATGAAGGCCACT	189
E E M S L L L V A M V K D Y V Q M K A T	63
GTGCTGGAGCAGGAGACAGAGGACTTCAGCATTGCAACACTCACCGAGAGATCCTGCAACACT	249
V L E Q E T E D F S I T T Q E R S C N T	83
<u>GCCATCTGTGTGACCCACAAGATGGCAGGCTGGCTGAGCAGATCTGGAGCGTGGTTAAG</u>	309
<u>A I C V T H K M A G W L S R S G S V V K</u>	103
AACAACTTCATGCCCATCAACATGGCTCCAAAGTCTGGCCGGCGCCGAGACAGCCT	369
N N F M P I N M G S K V L R R R R Q P	123
CAGGCCTGAGCTGTGAAATGACTCTAAAAAGAAGTGAACCTCAAGTTGCTTCACTGCAA	429
Q A *	125
AGTTGCTTCCCTGCAAATTAAAAGAACCAATTGAAAAATAGCATGGAAGACACACATA	489
TATGCATGCTTCTGCTTGAAATACAACCTTTTGCTTGAAACAAACTAACCTAAATGCA	549
GAATAAAATCATTGCAGTTACCTGA	574

Fig. 22

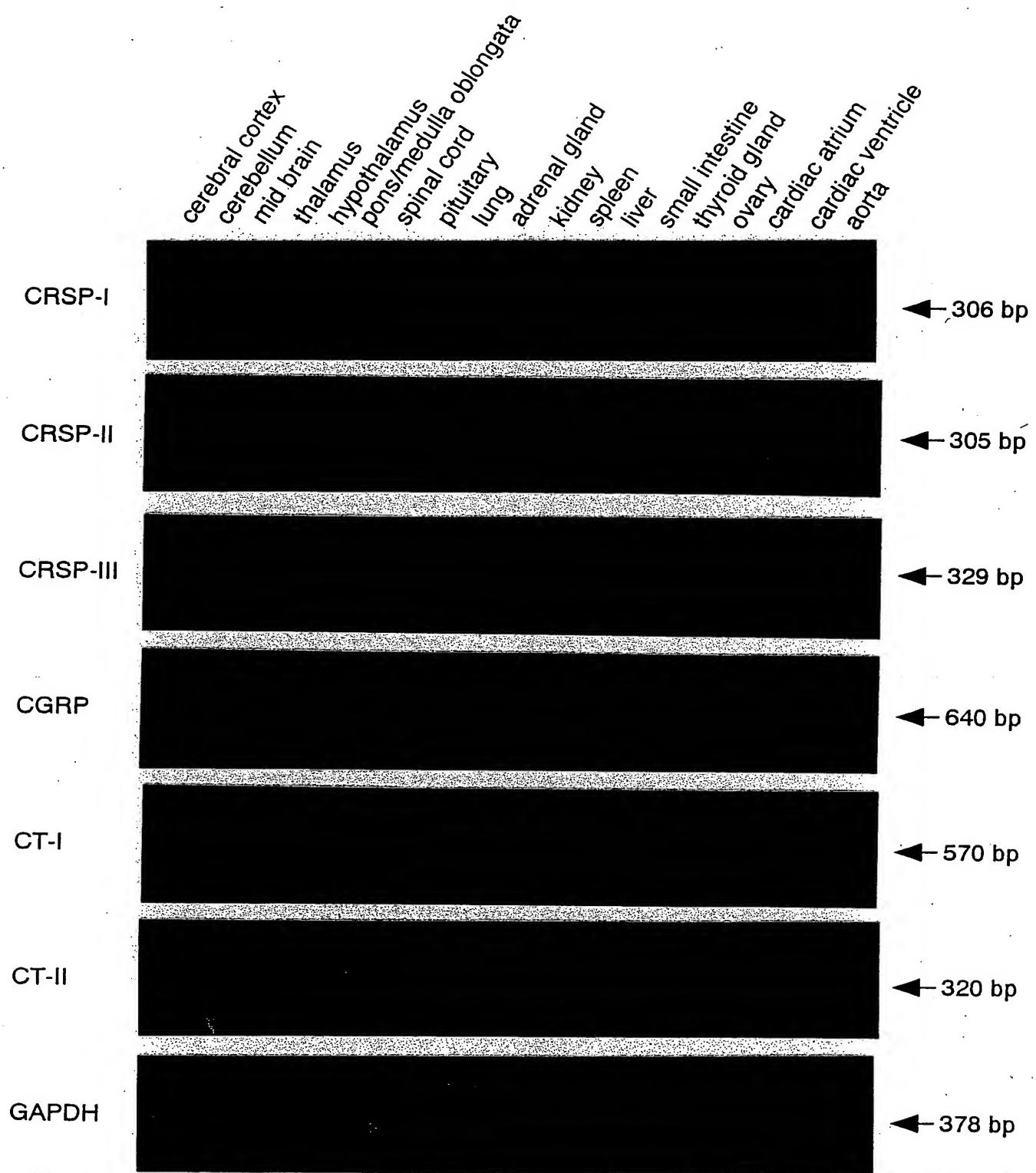
GCCCAGCTTACGTCTCCTTCTCGCCAGTGCATCACCTGCCACCAGCGCGTTGTC	-52
TTCTCCCACITGGCTCCAAGCTACCTGGTCTGCATCCAGAGGGCACCATGGCTTC	9
M G F	3
TGGAAGTTCCCCCCCCTCCTGATCCTCAGCATCCTGGTCTGTACCAAGCAGGAATGCTC	69
W K F P P F L I L S I L V L Y Q A G M L	23
CATGCCGCCATTCAAGGATGGCTTGGAAAGCAGCTTGATTCTGCCACACTCACGGAA	129
H A A P F R M A L G S S F D S A T L T E	43
GAGGAAATGTCCCTCCTACTGGTGCAATGGTAAGGATTATGTGCAGATGAAGGCCACT	189
E E M S L L L V A M V K D Y V Q M K A T	63
GTGCTGGAGCAGGAGACAGAGGACTTCAGCCTGGACAGCTCCAGAGCTAACAGTCAT	249
V L E Q E T E D F S L D S S R A K Q C N	83
AATCTGAGTACCTGTGTGGAACATATACATGGGACGTCAACAAGTTTATGCATT	309
N L S T C V L G T Y T W D V N K F Y A F	103
CCCTTAACTACAACGGATTAGAGTATCTGGCAAGAAATGGTCAGGGCCAGAGTCTCA	369
P L T T T G I R V S [REDACTED] K K W V R A R V S	123
GAGAAAGTCCATTATCCCTCAAGGCAGCATAACCTAAGGTGCTTAAGAAGGCCACCC	429
E K V H Y P S R Q H T L R C L R R P P P	143
CTCCTCTTCTAGTTCCCTCTCTAGAATTGCATGTGTTCTCTGGTTGCTCTGA	489
L L L S S S S P R I C M C S S L V A L	162
GCTGCTATCAGCAGCTTCCTTGTGGCATGGATGTCTGGAATATCAGAGAGGAGGTGGG	549
GGGTGGGGCAGGCAGGCCAGAAGAAAATCACTCAGGAATAGATTAGGAGAGAATGGCA	609
GCCCTGTGAGTGCCTGTGGATTACAGCAGAGCTCTCAGTCCTGCTCTGAACATGCT	669
TTTCACTAGGGAATAAAAGTAT	691

Fig. 23

SCNTASCVTHKMTGWI SRSGSVAKNNFMP-TNVD**SKIL**-NH₂
 SCNTAI**CVTHK**MAGWI SRSGSVVKNNFMP-TINM**GSKVL**-NH₂
 SCNTAT**CWTHRLV**GII SRSGSMVRSNLIP-TKM**GEKVG**-NH₂
 SCNTAT**CVTHRLA**GLI SRSGCMVKSNEVP-TDVGSEAF-NH₂
 YRQSMNNFOGLRSF**CCRFGTCTV**QKLAAHQIYQFTDKD**RGVAPRSKIS**PQGY-NH₂
 PCRSP-2
 PCRSP-3
 PCRSP
 PCGRP
 PAM

CSNLST**TCVLSAY**WRNLNNNEHREFSGM**GF**PETP-NH₂
 PE**CNNLSTCVL**GTYTWDVNKEYAEPLTTGIRVS-NH₂
 PCT
 PCT-2

Fig. 24



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